

**Amendments to the Claims:**

This listing of claims will replace all prior versions, and listings, of claims in the application:

1. (CURRENTLY AMENDED) A method of identifying gene expression regulation mechanisms in a genome comprising detecting, by computer, the connectron pairs that are symmetrically related and compete to effect gene expression regulation and outputting the result thereof to a user.

2. (CURRENTLY AMENDED) A method of identifying gene expression regulation mechanisms in a genome comprising detecting, by computer, the connectron pairs that are symmetrically related and cooperate to effect gene expression regulation and outputting the result thereof to a user.

3. (CURRENTLY AMENDED) A method of identifying gene expression regulation mechanisms in a genome comprising detecting, by computer, the connectron pairs that are asymmetrically related and compete to effect gene expression regulation and outputting the result thereof to a user.

4. (CURRENTLY AMENDED) A method of identifying gene expression regulation mechanisms in a genome comprising detecting, by computer, the connectron pairs that are asymmetrically related and

cooperate to effect gene expression regulation and outputting the result thereof to a user.

5. (CURRENTLY AMENDED) A method of designing gene expression regulation mechanisms in a genome comprising modeling, by computer, the connectron pairs that are symmetrically related and compete to effect gene expression regulation and outputting the result thereof to a user.

6. (CURRENTLY AMENDED) A method of designing gene expression regulation mechanisms in a genome comprising modeling, by computer, the connectron pairs that are symmetrically related and cooperate to effect gene expression regulation and outputting the result thereof to a user.

7. (CURRENTLY AMENDED) A method of designing gene expression regulation mechanisms in a genome comprising modeling, by computer, the connectron pairs that are asymmetrically related and compete to effect gene expression regulation and outputting the result thereof to a user.

8. (CURRENTLY AMENDED) A method of designing gene expression regulation mechanisms in a genome comprising modeling, by computer, the connectron pairs that are asymmetrically related and cooperate

to effect gene expression regulation and outputting the result thereof to a user.

9. (CURRENTLY AMENDED) A method of genome investigation, by computer comprising identifying a new class of connectrons that bind to the major groove of double-stranded DNA in two directions and outputting the result thereof to a user.

10. (CURRENTLY AMENDED) A method of genome investigation, by computer, comprising designing one or more new classes of connectrons that bind to the major groove of double-stranded DNA in two directions and outputting the result thereof to a user.

11. (CURRENTLY AMENDED) A method of genome investigation, by computer, comprising identifying the relationship between an existing pair of connectrons in a genome and outputting the result thereof to a user.

12. (CURRENTLY AMENDED) A method of genome investigation, by computer, comprising designing the relationship between a synthetic pair of connectrons in a genome and outputting the result thereof to a user.

13. (CURRENTLY AMENDED) A computer mediated method for identifying the relationship between an existing pair of connectrons in a genome that act in a competitive mode such that with respect to the individual connectrons there is an increased lifetime of connectron control of a set of genes and outputting the result thereof to a user.

14. (CURRENTLY AMENDED) a computer mediated method for designing a synthetic pair of connectrons in a genome that act in a competitive mode such that with respect to the individual connectrons there is an increased lifetime of connectron control of a set of genes and outputting the result thereof to a user.

15. (CURRENTLY AMENDED) A computer mediated method for identifying the relationship between an existing pair of connectrons in a genome that act in a cooperative mode such that with respect to the individual connectrons there is an increased lifetime of connectron control of a set of genes and outputting the result thereof to a user.

16. (CURRENTLY AMENDED) A computer mediated method for designing a synthetic pair of connectrons in a genome that act in a cooperative mode such that with respect to the individual connectrons there is an increased lifetime of connectron control of a set of genes and outputting the result thereof to a user.